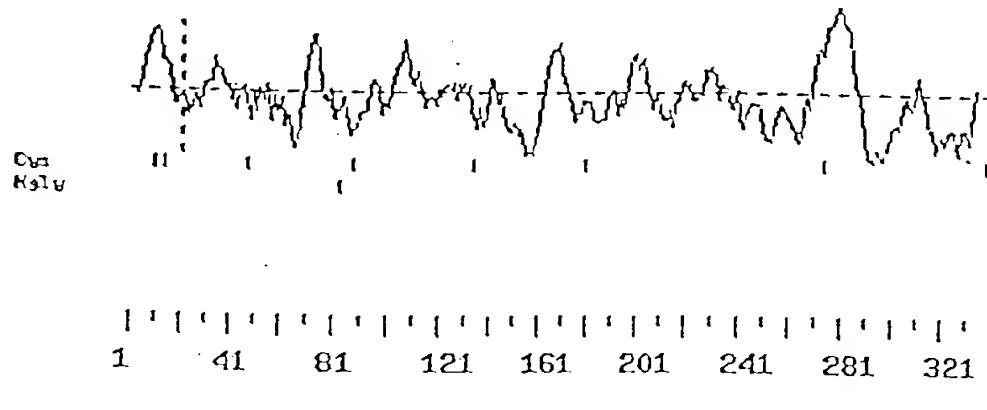


M	S	P	S	P	T	A	L	F	C	L		
GGAGTCGACCCACCGCTCCGCAGGGCTGAGGAACC	ATG	TCT	CCA	TCC	CCG	ACC	GCC	CTC	TTC	TGT	CTT	11
GGG	CTG	TGT	CTG	GGG	CGT	GTG	CCA	GCG	CAG	AGT	GGG	68
G	L	C	L	G	R	V	P	A	Q	S	G	31
GCT	CTG	CCC	ACC	TCC	CTG	GTG	CCC	CTG	GAG	CCA	GTG	128
A	L	P	S	S	L	V	P	L	E	K	P	51
GCT	CTG	CCC	ACC	TCC	CTG	GTG	CCC	CTG	GAG	CCA	GTG	188
P	G	V	D	L	Y	R	L	E	K	L	S	71
CCG	GGC	GTG	GAC	CTG	TAC	CGC	CTG	GAG	AAG	CTG	AGT	246
V	L	F	I	P	A	M	K	R	S	L	A	91
GTC	CTG	TTC	ATC	CCG	GCC	ATG	AAG	AGA	AGT	CTG	GCT	308
N	G	S	L	W	S	L	P	S	D	Q	L	51
AAC	GGG	AGC	CTC	TGG	TCC	CTG	CCC	AGC	GAC	CAG	CTG	368
A	K	P	S	L	S	A	Q	P	G	P	A	131
GCC	AAA	CCC	TCG	CTC	TCA	GCC	CAG	CCC	GGC	CCG	GTG	428
L	O	C	Q	T	R	Y	G	F	D	Q	F	151
CTA	CAG	TGT	CAG	ACT	CGG	TAT	GGC	TTT	GAC	CAA	TTT	488
A	P	Y	K	N	P	E	R	W	Y	R	A	171
GGC	CCC	TAC	AAG	AAT	CCC	GAG	AGA	TGG	TAC	CGG	GCT	548
A	A	H	S	G	T	Y	R	C	Y	S	F	191
GCC	GCC	CAC	AGC	GGG	ACC	TAC	CGA	TGC	TAC	AGC	TTC	608
S	A	P	S	D	P	L	E	L	V	V	T	211
TCG	GCC	CCC	AGC	GAC	CCC	CTG	GAG	CTT	GTG	GTC	ACA	668
L	P	T	E	P	P	S	S	V	A	E	F	231
TTA	CCA	ACA	GAA	CCA	CCT	TCC	TCG	GTA	GCA	GAA	TTC	728
V	S	F	T	N	K	V	F	T	T	E	T	251
GTC	TCA	TTC	ACA	AAC	AAA	GTC	TTC	ACA	ACT	GAG	ACT	788
K	E	S	D	S	P	A	G	P	A	R	Q	271
AAG	GAG	TCA	GAC	TCT	CCA	GCT	GGT	CCT	GCC	CGC	CAG	848
R	I	C	L	G	A	V	I	L	I	I	L	291
CGG	ATA	TGC	CTC	GGG	GCT	GTG	ATC	CTA	ATA	ATC	CTG	908
H	S	R	R	K	R	L	R	H	R	G	R	311
CAC	AGC	CGG	AGG	AAG	CGC	CTG	CGG	CAC	AGG	GGC	AGG	968
L	P	P	L	P	Q	T	R	K	S	H	G	331
CTG	CCG	CCC	CTC	CCG	CAG	ACC	CGG	AAA	TCA	CAC	GGG	1028
V	H	S	R	G	L	C	S	*				340
GTT	CAC	AGC	CGC	GGG	TTA	TGT	TCA	TGA				1055

FIGURE 1

CCGCTGAACCCAGGCACGGTGTATCAAGGGAGGGATCATGGCATGGGAGGCAGTCAAAGACTGGCGTGTGGAGC 1134
 CGTGGAAAGCAGGAGGGCAGAGGGCTACAGCTGTGAAACGAGGCCATGCTGCCTCCCTGGTGTTCATCAGGGAGCCG 1213
 TTGGGCCAGTGCTGCTGTCTGCTGCCTCTGCTGAGGGCACCCCTCCATTGGGATGAAAGGAATCTGTGGAGAC 1292
 CCCATCCTCCCTGCACACTGTGGATGACATGGTACCCGGCTGGACCACATACTGGCCTCTTCATCAACCTCTCT 1371
 AATATGGGCTCCAGACGGATCTAAGGTTCCAGCTCTAGGGTTGACTCTGTTCCATCTCTGTGCAAAATCTCTCT 1450
 GTGCTCCCTTGGCCCTCTGTCTCTGGTTTCCAGAAAACCTCTCACCCCTCACTCCATCTCCACTGGGTC 1529
 TAACAAATCTCCTTGTCTCTCAGAACGGGTCTGCAGGCAGTTGGGTATGTCAATTTCCTAGTGTAAAATCT 1608
 AGCACGTTGCCCTCCCTCACATTAGAAAAACAGATCAGCCTGTGCAACATGGTGAACCTCATCTTACCAACAA 1687
 AACAAAAAAACACAAAAATTAGCCAGGTGGTGGTGGCATCCCTATACTCCCAGCAACTGGGGGGCTGAGGTGGAGA 1766
 ATGGCTTGAGCCTGGGAGGCAGAGGTTGCACTGAGCTGAGATCACACCACTGCACTCTAGCTGGGTGACCAAGGCTGA 1845
 CCTTGCTCAAAAAATACAGGGATGAATATGTCAATTACCCGTATTGATCATAGCACGTTGATAACATGTACTGCAAT 1924
 ATTGCTGTCCACCCATAAAATATGTACAATTATGTATACTTTAAAAATCATAAAAATAGATAATGAAAAAAAAA 2003
 AAAAAAAAAAAGGGCGGGCGCTAGACTAGTCTAGAGAACAA 2047

FIGURE 1 cont.

**FIGURE 2**

ALIGN calculates a global alignment of two sequences
version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
> U91928 ORF 1893 aa vs.
> hT268 ORF 1017 aa
scoring matrix: paml20.mat, gap penalties: -12/-4
37.7% identity; Global alignment score: -8

10	20	30	40	50	60	70
inputs ATGACGCCCGCCCTCACAGGCCCTGCTGCCTGGCTGAGTCTGGCCCCAGGACCCGGTGCAGGCAG						
::: ::						
ATGTCTCCATCCCCGACCGCCCTTCTGTCTTGGCTGTCTGGGG-TGTGCCAGC-GCAGAGTG						
10	20	30	40	50	60	
80 90 100 110 120 130						
inputs GGCCTTCCCCAAACCCACCCCTGGCTGAGCCAGGCTCTGTAT-CAGCTGGGGAGCCCCGTGACCA						
::: ::						
GACCGCTCCCCAAGCCCTCCCTCCAGGCTCTGCCAGCTCCCTGGTGCCTGGAGAAGCCA-GTGAACC						
70	80	90	100	110	120	130
140 150 160 170 180 190 200						
inputs TCTGGTGTCAAGGGAGCCTGGAGGCCAGGACTACCGACTGGATAAAGAGGGAAAGCCAGAGCCCCTTGGA						
::: ::						
TCGGGTGCCAGGG--ACCT----CCGGGCGTG--GACCTGTA-----CCGCCTGGAG----AAG						
140	150	160	170	180	190	180
210 220 230 240 250 260 270						
inputs CAGAAAATAACCCACTGGAACCCAAAGAACAGGCCAGATTCTCATCCATCCATGACACAGCACCATGGC						
::: ::						
CTGAGTT--CCAGCAGGTACC-AGGATCA-GGCAGTCTCTCATCCGCCATGAAGAGAAGTCTGGCT						
190	200	210	220	230	240	
280 290 300 310 320 330 340						
inputs GGGAGATACCGCTGCCACTATTACAGCTGGCAG--GCTGGTCAGAGCCCAGGGACCCCTGGAGCTGGT						
::: ::						
GGACGCTACCGCTGCTCTAC--CAGAACGGAGCCTGGTCCCTGCCAGGGACCAGCTGGAGCTCGT						
250	260	270	280	290	300	310
350 360 370 380 390 400 410						
inputs GATGACAGGATTCTACAACAAACCCACCCCTCTCACGCCCTGCCAGCCCTGTGGTGGCCTCAGGGGGAAAT						
::: ::						
TCCCACGGGAGTTTGCCAAACCCCTCGCTCTCACGCCAGGCCGGCCGGGGTGTGTCAGGAGGGGAC						
320	330	340	350	360	370	380
420 430 440 450 460 470 480						
inputs ATGACCCCTCCGATGTGGCTCACAGAACGGATATCACCATTTGTTCTGTATGAAGGAAGGAGAACACCAGC						
::: ::						
GTAACCCCTACAGTGTCAAGACTCGGTATGGCTTGACCAAATTGCTCTGTACAAGGAAGG-----						
390	400	410	420	430	440	
490 , 500 510 520 530 540 550						
inputs TCCCCCGGACCCCTGGACTCACAGCAGCTCCACAGTGGGGGTTCAGGCCCTGTGGCCCCG						
::: ::						

FIGURE 3

-----GGACCCCTG----- C---GCCCTA-----CAA
 450
 560 570 580 590 600 610 620
 inputs GAACCCCAGCCACAGGTGGAGGTTCACATGCATTACTATTATGAACACCCCCCAGGTGTGGTCCCAC
 :::: ::::: ::::: ::::: ::::: ::::: :::
 GAATCCCCA-----GAGATGGTAC-CGGGCTAGT- TT----- CCCCAT----- CAT
 470 480 490 500
 630 640 650 660 670 680 690
 inputs CCCAGTGACCCCCCTGGAGATTCTGCCCTCAGGCCTGTCTAGGAAGCCCTCCCTCTGACCCCTGCAGGGCC
 ::::::: :::::::
 CACGGTGACCGCC-----GCCACAG-----
 510 520
 700 710 720 730 740 750 760
 inputs CTGTCCCTGGCCCCCTGGGCAGAGCCTGACCCCTCCAGTGTGGCTCTGATGTCGGCTACGGACAGATTGTTCT
 ::::::: ::::::: ::::::: :::::::
 CGGAACCTA-----CCGATG----- CTACAGC----- TTCT
 530 540 550
 770 780 790 800 810 820 830
 inputs GTATAAGGAGGGGAACGTGACTTCCCTCCAGCCCCCTGGCCAGCAGCCCCAGGCTGGGCTCTCCAGGCC
 :::::::
 -----CCAGCAG-----
 840 850 860 870 880 890 900
 inputs AACTTCACCCCTGGCCCCCTGTGAGCCCCCTCCCAGGGGGCCAGTACAGGTGCTATGGTGCACACAACCTCT
 :::::::
 -----GGACCCA----- TACCT--
 560
 910 920 930 940 950 960 970
 inputs CCTCCGAGTGGTCGGCCCCCAGCGACCCCTCAACATCCTGATGGCAGGACAGATCTATGACACCGTCTC
 ::::::::::::: ::::: :::::
 -----GTGGTCGGCCCCCAGCGACCCCTGG----- GCT----- TGTG-----
 570 580 590 600
 980 990 1000 1010 1020 1030 1040
 inputs CCTGTCAGCACAGCCGGCCCCACAGTGGCCTCAGGAGAGAACGTGACCCCTGCTGTGTCAGTCATGGTGG
 ::::: ::::: :::::::
 ---CTCA-----CAGGAACCTCTGTGACC----- CCCAGC----- CGGT-----
 610 620 630
 1050 1060 1070 1080 1090 1100 1110
 inputs CAGTTGACACTTCCTCTGACCAAAGAAGGGCAGCCCACCCCCACTGCGTCTGAGATCAATGTACG
 ::::::: ::::: :::::::
 -----TACCAACAGAAC----- CA---CCTTCC----- TCG
 640 650
 1120 1130 1140 1150 1160 1170 1180

FIGURE 3 cont.

Inputs GAGCTCATAACTTACCAAGGCTGAATCCCCATGAGTCTGTGACCTCAGCCCACGGGGGACCTACAGGTG
 :... ::::::: :
 CTA-----GCAGAATTCTC-----AGAACCCAC----CGCTGA----ACTG--A
 660 670 680 690
 1190 1200 1210 1220 1230 1240 1250
Inputs CTACGGCTCATACAGCTCCAAACCCCCATGCTGTCTTCCCCAGTGAGCCCCCTGGAACTCATGCTCTCA
 :
 C-----GGCTCATTC-----GAAAC-----AAAGTCTT-----CACAC-----CTGAGACT-----TCT--
 700 710 720 730
 1260 1270 1280 1290 1300 1310 1320
Inputs GGACACTCTGGAGGCTCCAGCCTCCCACCCACAGGGCCGCCCTCCACACCTGGTCTGGGAAGATACTGG

 -----AGGAGTATC--ACCACCAAGTCCAAAGGA--GTCAGACTCTCCAG--CTGG-----
 740 750 760 770
 1330 1340 1350 1360 1370 1380 1390
Inputs AGCTTTGATTGGGGTCTGGTGGCCTTCGTCCTGCTCTCCCTCTCTCTCTCTCCGACGG
 :::::
 -----TCCTGC-----CCGGCAGTA---CTACACCAAGG
 780 790 800
 1400 1410 1420 1430 1440 1450 1460
Inputs TCAGCGTCACAGCAAAACACAGGACATCTGACCAAGAGAAAGACTGATTCCAGCGTCTGCAGGGGCTGCG
 :
 GCAAAC-----CTGGTC-----CGGATAT--GCCTC---GGGGCTG--
 810 820 830
 1470 1480 1490 1500 1510 1520 1530
Inputs GAGACAGAGCCAAGGACAGGGCCCTGAGGAGGTCCAGCCAGCTGCTGACGTCCAGGAAGAAAACC

 -----TGATCTAAATAA-----TCCTG--GGGGGTTCTG-----CCAGA-GGACTGG-----C
 840 850 860 870
 1540 1550 1560 1570 1580 1590 1600
Inputs TCTATGCTGCCGTGAAGGACACACAGTCTGAGG-ACAGGGTGGAGCTGGACAGT-CAGAGCCCACACGAT

 AC-----AGCG--GAGGAAGCGC--CTGGCCACAGGG---GCAGGGCTGTGCAGAGGCCGCT---
 880 890 900 910 920
 1610 1620 1630 1640 1650 1660 1670
Inputs GAAGACCCCCAGGGAGTGACGTATGCCCGGTGAAACACTCCAGTCCTAGGAGAGAAATGGCTCTCCTC

 -----TCC-----GCCCTG-----CCGC---C
 930 940
 1680 1690 1700 1710 1720 1730 1740
Inputs CCTCCTCACTGCTGGGAATTCTGGACACAAAGGACAGACAGGTGGAAGAGGGACAGGCAGATGGACAC
 :::::
 CCTCC-CGCAGAC-----CCGAAATCA---CA---CGGG-----GGTCAGG---ATGGA---
 950 960 970 980

FIGURE 3 cont.

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 1750      1760      1770      1780      1790      1800      1810
inputs TGAGGGCTGCTGCATCTGAAGCCCTCCCAGGATGTGACCTACGCCCGACTGCAACAGCTTGACCCCTTACAGCCTA
       :::::    :::::    :::::::    :::::::    :::::::    :::::::    :::::::
       ---GGC---- CGAC----- AGGATGTT----- CACAGC----- CG-
       990                      1000

 1820      1830      1840      1850      1860      1870      1880
inputs AAGGCAACTGACCCTCCTCCATCCCAGGAAGGGAACCTCCAGCTGAGCCCAGCATCTACGCCACTCTGG
       :::::::    :::::::    :::::::    :::::::    :::::::    :::::::    :::::::
       ---CGGGTTATG----- TTCA-----
       1010

 1890
inputs CCATCCAC

```

FIGURE 3 cont.

ALIGN calculates a global alignment of two sequences
 version 2.0. Please cite: Myers and Miller, CABIOS (1989)
 > hT268 a.a. 339 aa vs.
 > GenPept U91928 - Human clone HL9 monocyte inhib 631 aa
 scoring matrix: pam120.mat, gap penalties: -12/-4
 23.0% identity; Global alignment score: -642

	10	20	30	40	50	60	
inputs	MSPSPTALPCLGLCIG-RVPAQSGPLPKPLQLALPSSIVPLEKPVTLRQCQGPIQNTILYRLDKLSSS- MTPALTAIICLGLSLGPRTRVQAGPFPKPTLWAEPGSVISWGSPVTIWCQGSLEAQSBYRILDKEGSPEPLD						
	10	20	30	40	50	60	70
	70	80	90	100	110	120	130
inputs	RYQ-----DQAVLFIPAKMRSLAGRYRCSYQNGLSWSLPSDQLELVATGVFAFPSLSAQPGPAVSSGGDV RNNPLEPKNARFSIPSMTENHAGGRYCHYYSSAGWSEPSDPLELVMTCGFYNPTL SALPSPVVASGGNM						
	80	90	100	110	120	130	140
	150	160	170	180	190	200	210
	140	150					
inputs	-----TIIQCQT-----T.Y.----- TLRCGSQKGYHHFVLMKEGEHQLPRTLDSQQLHSGGFQALFPVGPVNPSPHRWAFTCYYYYYANTPQVWSHP						
	150	160	170	180	190	200	210
	220	230	240	250	260	270	280
	140	150					
inputs	-----GFDQFALYKEGDP----- SDPLEILPSGVSRSKPSLLTLQGPVLAPGQSLTLQCGSDVGYDRFLVLYKEGERDFLQRPGQQPQAGLSQAN						
	220	230	240	250	260	270	280
	160						
inputs	-----APYK-----NP-----ERW-- FTLGPVSPSHGGQYRCYGAHNLSEWSAPS DPLNILMAGQIYDTVSLSAQPGPTVASGENVTLLCQSQWWQ						
	290	300	310	320	330	340	350
	170	180	190	200			
inputs	-----YRASFPIITVTAHSGTYRCYSFSSRDPYLWSAPS DPLELVVTG FDTFLLTKEGAAHFFLRLRSMYGAHKYQAEPHPSPVTSAAHAGTYRCYGSYSSNPILLSFPSEPLELMVSG						
	360	370	380	390	400	410	420
	210	220	230	240	250	260	
inputs	TSVTFSRILPTEPPSS--VAEFSEATAELTVSFTNKVF-----TTETSRISITSPKESD--SPAGPA- HSGGSSLPPTPGPPSTPGLGRYLEVLIGVSVAFVLLLFLLLFLLRRQRHSKHRTSDQRKTDFQRPAAGAAE						
	430	440	450	460	470	480	490
	270	280	290				
inputs	RQYYTKGNLVRICLGAIVL---IILAGFLAEDW-----HSRRKR-- -----						

FIGURE 4

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500	510	520	530	540	550	560
TEPKDRGLLRRSSPAADVQEENLYAAVKDTQSEDRLVELDSQSPHDEDPQAVTYAPVKHSSPRREMASPPS inputs -----LRHRGRAVQ--RPL-----PPLPPLPQTRK-----SHGGQDGGQRQDVHSRGLC : . SLSGEFLDTKDRQVEEDRQMDTHEAAASEASQDVTYAQLHSLTLRRKATEPPPSQEGEPPAEPsiYATLAI 570 580 590 600 610 620 630						
inputs S						

FIGURE 4 cont.

Alignments of top-scoring domains:

tg: domain 1 of 2, from 41 to 90: score 4.1, E = 6.1

*->GesvtLtcsvsgfgppgvsvtWvfknngk.lgpsllgysysrlesgek

hT268 41 EKPVTLRCQGP-----PGVDLY-RLEK1SSS-----RYQDQ-- 70

anlsegrfsissltLtissvekeDsGtYtCvv<-*

++L i +++ +G Y+C

hT268 71 -----AVLFIPAMKRSLAGRYRCSY 90

FIGURE 5A

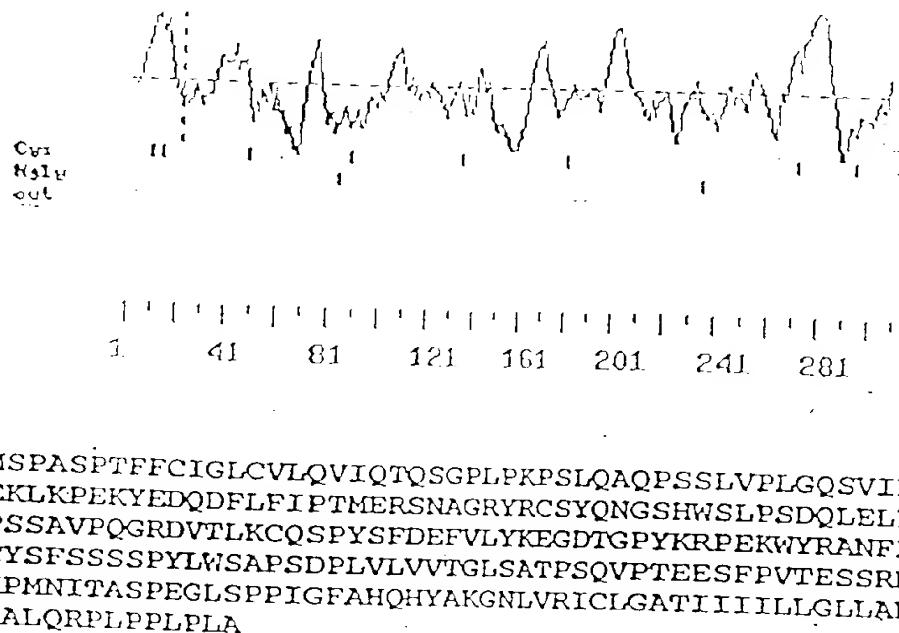
ig: domain 2 of 2, from 127 to 182: score 19.1, E = 0.1
 *->GesvtLtCsvsgfgppgvsvtWfyfngk.lgpsllgysysrlesgek
 G++vtL+C++ + ++ Y k+g++ + y++
 hT268 127 GGDVTLQCQTR--YGFDQFALY-KEGDpAP-----YKNPERWYR-- 167

anlseggrfsissltLtissvekeDsGtYtCvv<-
 +++i++v++ sGtY+C
 hT268 163 -----ASFPIITVTAAHSGTYRCYS 182

FIGURE 5B

GAGTCGACCCACCGTCCGTTCCCTGTTGCCACATAGCTCAGGACTGGGTTCAGAAC	M	S	P	A	4																
ATG TCT CCA CCC					74																
TCA CCC ACT TTC TTC TGT ATT GGG CTG TGT GTA CTG CAA GIG ATC CAA ACA CAG AGT GGC	S	P	T	F	F	C	I	G	L	C	V	L	Q	V	I	Q	T	Q	S	G	24
CCA CCC CCT AAC CCT TTC CTC CGG CTG CTG CCT GAA GTC GAA GCA GAG AGT GGC	P	L	P	E	P	S	L	Q	A	Q	I	S	L	V	P	L	G	Q	S	G	134
GTT ACT CGG AGG TGC CAG GGA CCT CCA GAT GTG GAT TTA TAT CGG CGG GAG AAA CTG AAA	V	I	L	R	C	Q	G	P	I	D	V	I	L	Y	E	L	P	R	L	F	64
CCG GAG AAG TAT GAA GAT CAA GAC TTT CTC TTC ATT CCA ACC ATG GAA AGA AGT AAT GCT	P	H	R	Y	E	D	O	D	E	L	F	I	P	T	H	E	H	S	N	I	314
GGA CGG TAT CGA TGC TCT TAT CAG AAT GGG AGT CAC TGG TCT CTC CCA AGT GAC CAG CTT	G	H	Y	R	C	S	Y	Q	N	G	S	H	W	S	L	P	S	D	Q	I	104
GAG CTA ATT GCT ACA GGT GTC ATT GTC AAA CCT TCA CTC TCA GCT CAT CCC AGT GCA GTC	E	L	I	A	T	G	V	Y	A	R	P	S	L	S	A	R	P	S	S	I	124
GTC CCT CCA GGC AGG GAT GTC ACT CCT AAG TGT CAG AGG CCA TAT AGT TTT GAT GAA GTC	V	I	Q	G	R	D	V	T	I	E	C	C	S	I	Y	S	I	D	E	F	434
GTT CTA TAC AAA GAA GGG GAT ACT GGG CCT TAT AAG AGA CCT GAG AAA TGG TAC CGG GGC	V	L	Y	K	E	G	D	T	G	I	Y	E	R	P	E	H	W	Y	R	A	164
AAT TTC CCC ATC ATC ACA GTG ACT GCT GCT CAC AGT GGG ACG TAC CGG TGT TAC AGC TTC	N	F	P	I	I	T	V	T	A	A	H	S	G	T	Y	R	C	Y	S	F	554
TCC AGG TCA TCT CCA TAC CTG TGG TCA GCC CCG AGT GAC CCT CTA GTG CTT GIG GTC ACT	S	S	S	P	Y	L	W	S	A	P	S	D	P	L	V	L	V	V	T	184	
GGA CTC TCT GCC ACT CCC AGC CAG GTA CCC ACG GAA TCA TTT CCT GTG ACA GAA TCC	G	L	S	A	T	P	S	Q	V	P	T	E	E	S	F	P	V	T	E	S	674
TCC AGG AGA CCT TCC ATC TTA CCC ACA AAC AAA ATA TCT ACA ACT GAA AAG CCT ATG AAT	S	R	R	P	S	I	L	P	T	N	K	I	S	T	T	F	E	P	M	N	734
ATC ACT GCC TCT CCA GAG GGG CTG AGC CCT CCA ATT GGT TTT GCT CAT CAG CAC TAT GCC	I	T	A	S	P	E	G	L	S	P	P	I	G	F	A	H	Q	H	Y	A	264
AAG GGG AAT CTG GTC CGG ATA TGC CTT GGT GCC ACG ATT ATA ATA ATT TTG TTG GGG CTT	K	G	N	L	V	R	I	C	L	G	A	T	I	I	I	I	L	L	G	L	854
CTA CCA GAG GAT TGG CAC AGT CGG AAG AAA TGC CTG CAA CAC AGG ATG AGA GCT TTG CAA	L	A	E	D	W	H	S	R	K	R	C	L	Q	H	R	M	R	A	L	Q	914
AGG CCA CTA CCA CCC CTC CCA CTG GCC TAG	R	P	L	P	P	L	P	L	A	*										304	
AGG CCA CTA CCA CCC CTC CCA CTG GCC TAG																				974	
AAATAACTTGGCTTCAGCAGAGGGATTGACCAGACATCCATGCACAAACCATGGACATCACCACTAGAGCCACAGACAT																				314	
GGACATACTCAAGAGTGGGGAGGTATATAAAAAAAATGAGTGTGGAGAATAAAATGCAGAGCCAACAAGGTGAAAAAAA																				1083	
A																				1162	
																				1163	

FIGURE 6



MSPASPTFFCIGLCVLQVIQTQSGPLPKPSLQAQPSSLVPLGQSVILRCQGPPDVDLYRL
EKLKPEKYEDQDFLFIPTMERSNAGRYRCSYQNGSHWSLPSDQLELIATGVYAKPSSL
PSSAVPQGRDVTLKCQSPYSFDEFVLYKEGDTGPYKRPEKWYRANFPIITVTAHSGTYR
CYSFSSSSPYLWSAPSDPLVLTGSLATPSQVPTTEESFPVTTESSRRPSILPTNKISTTE
KPMNITASPEGLSPIGFAHQHYAKGNLVRICLGATIIIIILLGLLAEDWHSRKKCLQHRM
RALQRPLPPLPLA

FIGURE 7

FIGURE 8

--CCGGA-----CA-----AGTATGAAGATCAAGAC---TTTCTCTT-----CATT-
 200 210 220
 560 570 580 590 600 610 620
 Input 6 ACCCCAGCCCACAGGTGAGGTTCACATGCTATTACTATTATGAAACACCCCCCAGGTGTGGTCCCACCC
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
 ::::: CCAACCATGGAAANAACTAATGCTAATGCTGAGACCGATCTATGCT
 130 140 150 160 170 180 190
 630 640 650 660 670 680 690
 Input 6 CAGTGACCCCCCTGAGAGATTCTGGGCTTCAGGGGIGTAGGAAGCCCCCTCCCTCTGACCCCTGCAGGGCCCT
 ::::: ::::: ::::: ::::: ::::: ::::: :::::
 CGATG---CTCTTA-----TCAGA-----ATGGGAGTC-----ACTGGTCTCT
 270 280 290
 700 710 720 730 740 750 760
 Input 6 CTCCTGGCCCCCTGGGACAGAGCCTGACCUCTCCAGTGTGGCTCTGATGTCGGCTACGGACAGATTTGTTCTGT
 ::::: ::::: ::::: ::::: ::::: :::::
 ::::: COCAG --- GAGGAGCTTGAG-----CTAATT---GCTAC---GCTAC
 300 310 320
 770 780 790 800 810 820 830
 Input 6 ATAAGGAGGGGGAACGTGACTTCCTCCAGGCCCTGGCCAGCAGCCCCAGGCTGGCTCTCCCAGGCCAA
 ::::: ::::: ::::: :::::
 ---AGGTGTGTATGCTAAAC--CCTC-----ACTCTC-----
 330 340 350
 840 850 860 870 880 890 900
 Input 6 CTTCACCCCTGGCCCCCTGTGAGCCCCCTCCACGGGGGCCAGTACAGGTGCTATGGTCACACAACCTCTCC
 ::::: ::::: :::::
 ---AGCTCATCCCA-----GCT-----
 360
 910 920 930 940 950 960 970
 Input 6 TCCGAGTGGTGGCCCCCAGCGACCCCCCTGAAACATCCTGATGGCAGGGACAGATCTATGACACCGTCTCCC
 ::::: ::::: ::::: ::::: ::::: :::::
 ---CAGCAGTCCC-----TC---AAGGCAGG---GAT---GTGACTCTGA-----
 370 380 390 400
 980 990 1000 1010 1020 1030 1040
 Input 6 TGTCAAGCACAGCCGGCCCCAACGTGGCTCAGGAGAGAACGTGACCCCTGCTGTCACTGAGATCAATGTACGGA
 ::::: ::::: ::::: :::::
 AGT-----GCCAGAGCCCCATA-----CAGTTTGATGA--
 410 420
 1050 1060 1070 1080 1090 1100 1110
 Input 6 GTTGACACTTCTCTGACCAAAGAAGGGCAGCCCACCTCCCCACTGCGTCTGAGATCAATGTACGGA
 ::::: ::::: ::::: ::::: ::::: :::::
 ---ATTCGTTCTATAACAAAAGAAGGGG-----AT-----ACTGGGCCTTATA--AGAGACCTGA
 430 440 450 460 470
 1120 1130 1140 1150 1160 1170 1180

FIGURE 8 cont.

FIGURE 8 cont.

1750 1760 1770 1780 1790 1800 1810
inputs GCTGCTGCATCTGAAGCCTCCCAGGATGTGACCTACGCCAGCTGCACAGCTTGACCCCTAGACGGAAAGG
:: : :: : .
GC--CTGCAACA-----CAGGATGAGA-----GCTTTGC-----AAGGG
890 900 910

1820 1830 1840 1850 1860 1870 1880
inputs CAACTGAGGCTCTCCATCCCCAGGAAGGGAAACCTCCAGCTGAGGCCAGCATCTAGCCACTCTGGCCAA
: : : .
CCACTA-----CCACC-----CCTCC-----CACTGGCC--
920 930

1890
inputs CCAC

FIGURE 8 cont.

FIGURE 9

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TEPFQGILRHSQPAADVQERNLYAAVKDTQSEDRAVLEIDSQSPHDEDPQAVTYAIYAHSSPRREMASPPG
500 510 520 530 540 550 560

280 290 300 310
input6 CLGATIIIILLGLLAEDWH-----SRKKCLQHRMRALQRPL----PP-----LPL
...
SLSGFLOTKDPROVEEDRQMDTEAAASEASQDVTYAQLHSLTLLRKATEPPPSQEGERPAPSIYATLAI
570 580 590 600 610 620 630

Input6: 7

B:

FIGURE 9 cont.

Alignments of top-scoring domains:
1g: domain 1 of 2, from 42 to 91; score 10.2, E = 1.4

*->GesvtLtcsvsgfgppgvsvtWvfknk.lgpsllgysysrlesgek
mT268 42 G+sv L+C+ ++v Y + k ++ +++e +
 GQSVIIRCQGP-----PDVDLY-RIEKIKP-----EKYEDQ-- 71
anlsegrfaissltltissavekeDsGtYtCvv<- *
mT268 72 L i + e+++G Y+C
 -----DFLPIPTMERSNAGRYFCSY 91

FIGURE 10A

fig: domain 2 of 2, from 128 to 183; score 9.6, E = 1.6
*->GesvtLtcsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek
rT268 128 G +vtL C++ + y k+g++ + Y+r+e +
GRDVTLKCQSP---YSFDEFVLY-KEGDtGP-----YKRPEKw-Y 162
anlsegrfsissltLtissvekeDsGtYtCvv<- *
rT268 163 RA-----NFPIITVTAAHSGTYRCYS 183

FIGURE 10B

ALIGN calculates a global alignment of two sequences

Please cite: Myers and Miller, CABIOS (1988)

≥ hT268 c.c.

(2383)

BT268 B

333 88

SCORING MATRIX NO. 120

Scoring Matrix: Pamp20.mat, gap penalties: -12/-6/-4/-2/-1

64.4% identity; Global alignment score: 1011

	10	20	30	40	50	60
inputs	HSPSPTALFCLGLCLGRV-P	QSGPLWPSLQALPSSLVPL	EKPVTLRCQQPPGV	DLYRLEKLSSRYQD		
:..:..:..: ..	: ..:..:..:..:..:..::..:..:..:..:..::..:..:..:..:..::..:..:..:..:..::..:..:..:..:..: ..
	HSPASPTFFCIGLCVLQVQI	QSGPLPFSLQAPSSLVPLGQ	SVILRCQQPPDV	DLYRLEKLKEPKYHD		
	10	20	30	40	50	60

70	80	90	100	110	120	130	
inputs CAVLFIPAKKESLAGRYRCYQNGSLWLSLPSDQLELIVATGVFAF PSLSAQIIGPAVSSGGDVTLHQCTRYG							
.. ::::: ::							
QDFLFIFTHERSHAGRYRCYQNGSHWSLPSDQLELIATGVYAF PSLSAHFSSAVPQGRDVTLNCQSPYS	80	90	100	110	120	130	140

140 150 160 170 180 190 200
 inputs FDQFALYKEGDPAPYKPNPERWYRASFPPIITVTAAHSGTYRCYSFSSRDPYLWSAPSDFELVVVTGTSVTP
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
 FDEFVLYKEGDTGPYKRPEKHYRANFPPIITVTAAHSGTYRCYSFSSSPYLWSAPSDFPLVLVVVTGLSATP
 150 160 170 180 190 200 210

210 220 230 240 250 260 270
 inputs SRLPTEPSSVAEFSEATAELTVSFTNKFVTTETSRSPKESDSPAGPARQYYTKGNLVRICLGAVI
 : . . . : . . : .
 SQVPTEESFPVTESSRTPSILP---TNKISTTEKPMNITASPEGLSPPIGFAHQHYAKGNLVRICLGATI
 220 230 240 250 260 270

280	290	300	310	320	330
inputs LIILAGFLAEDWHSRRKRLRHRGRAVQRPLPPLPQTRKSHGGQDGGRQDVHSRGIC : ..::: ..::: ..::: ..::: ..::: ..::: ..::: ..::: ..::: ..					
IIILLGLAEDWHSRKKCLQHMRMALQRPLPPLP-LA-----					
280	290	300	310		

FIGURE 11

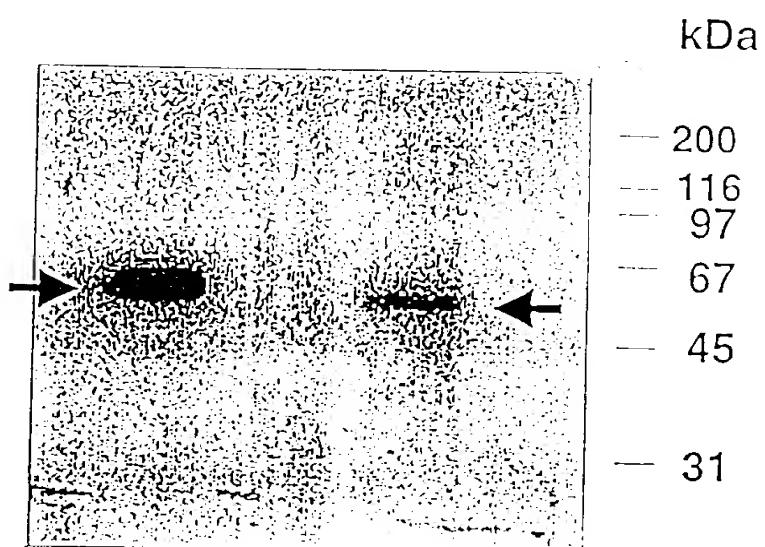


FIGURE 12

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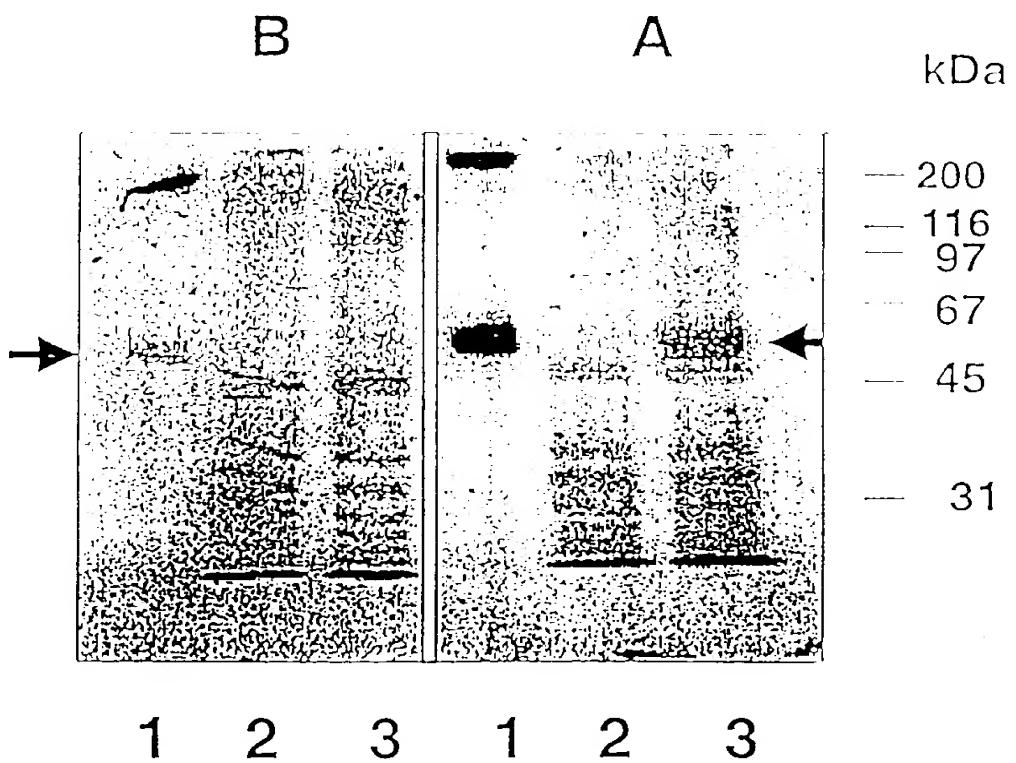
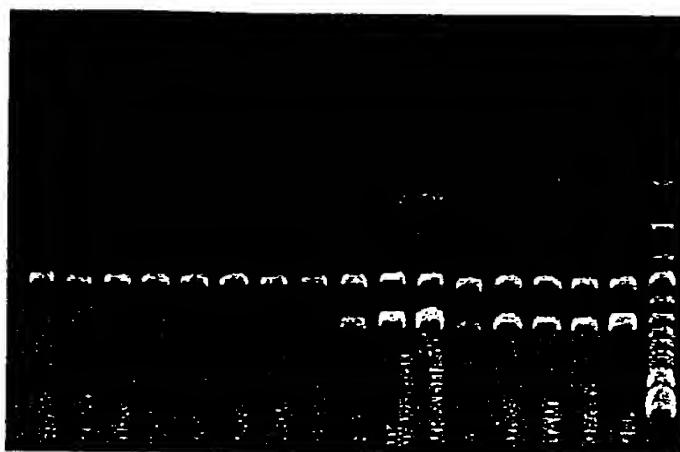


FIGURE 13



Sp LN Thy PBL BM FL

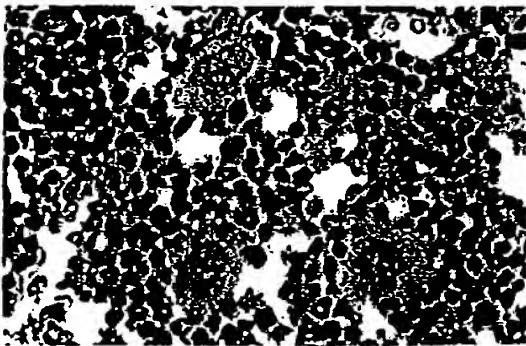
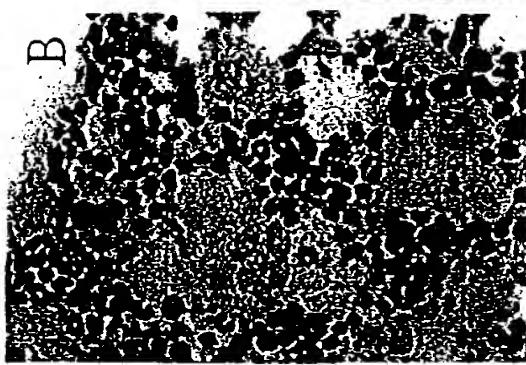
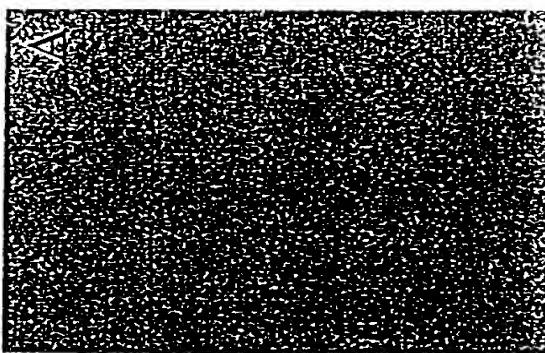
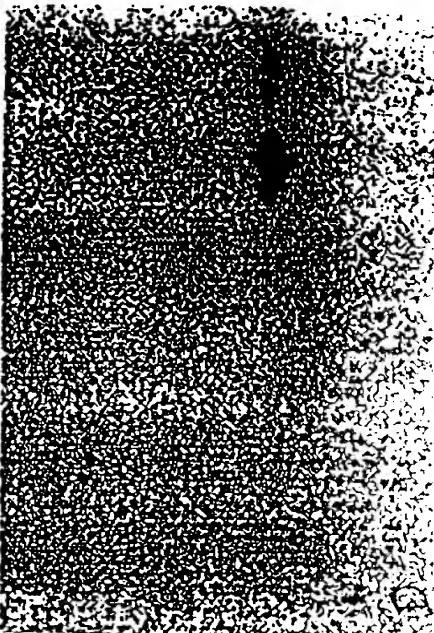
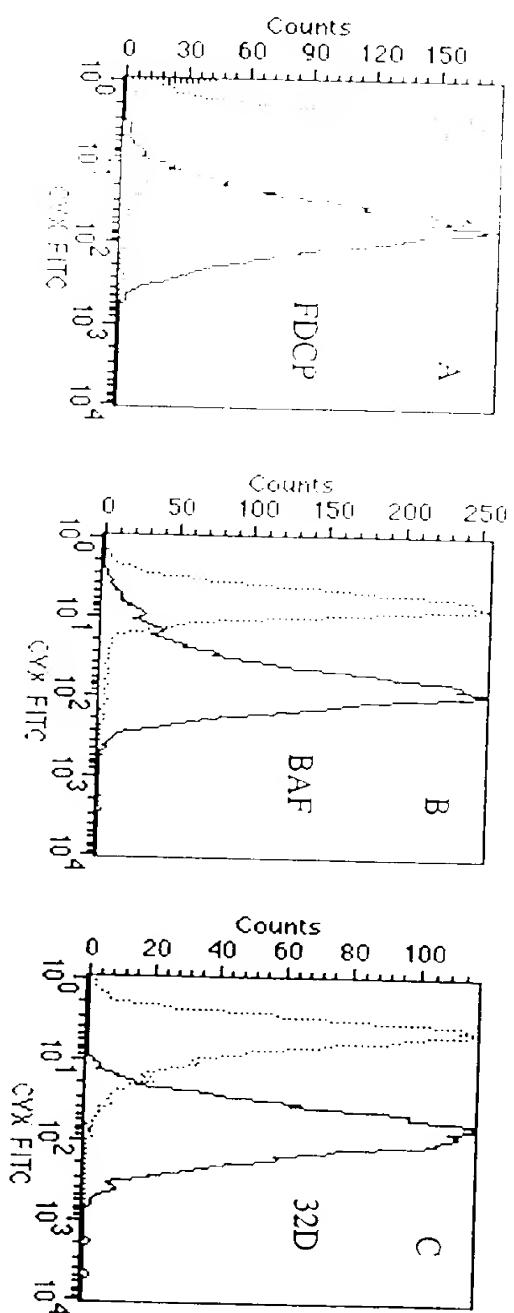


FIGURE 14

**FIGURE 15**

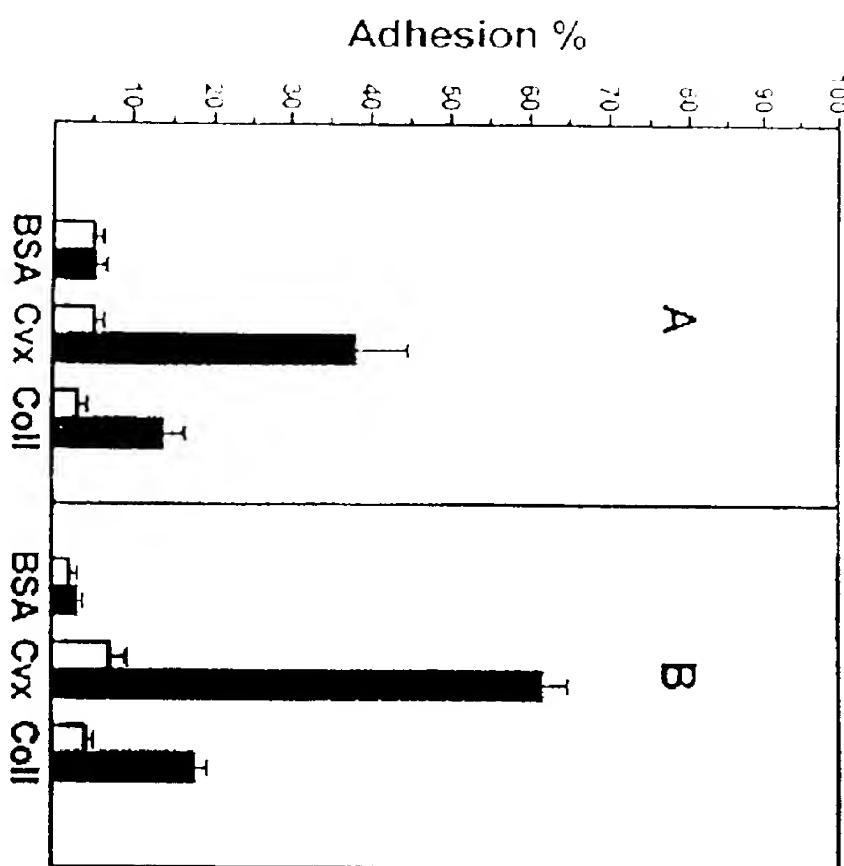


FIGURE 16

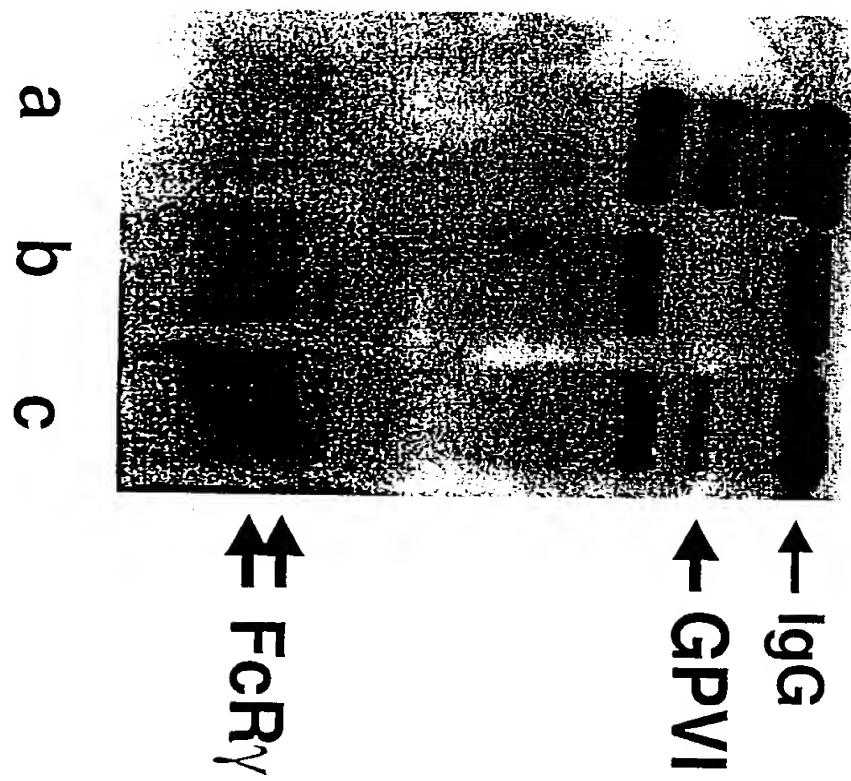
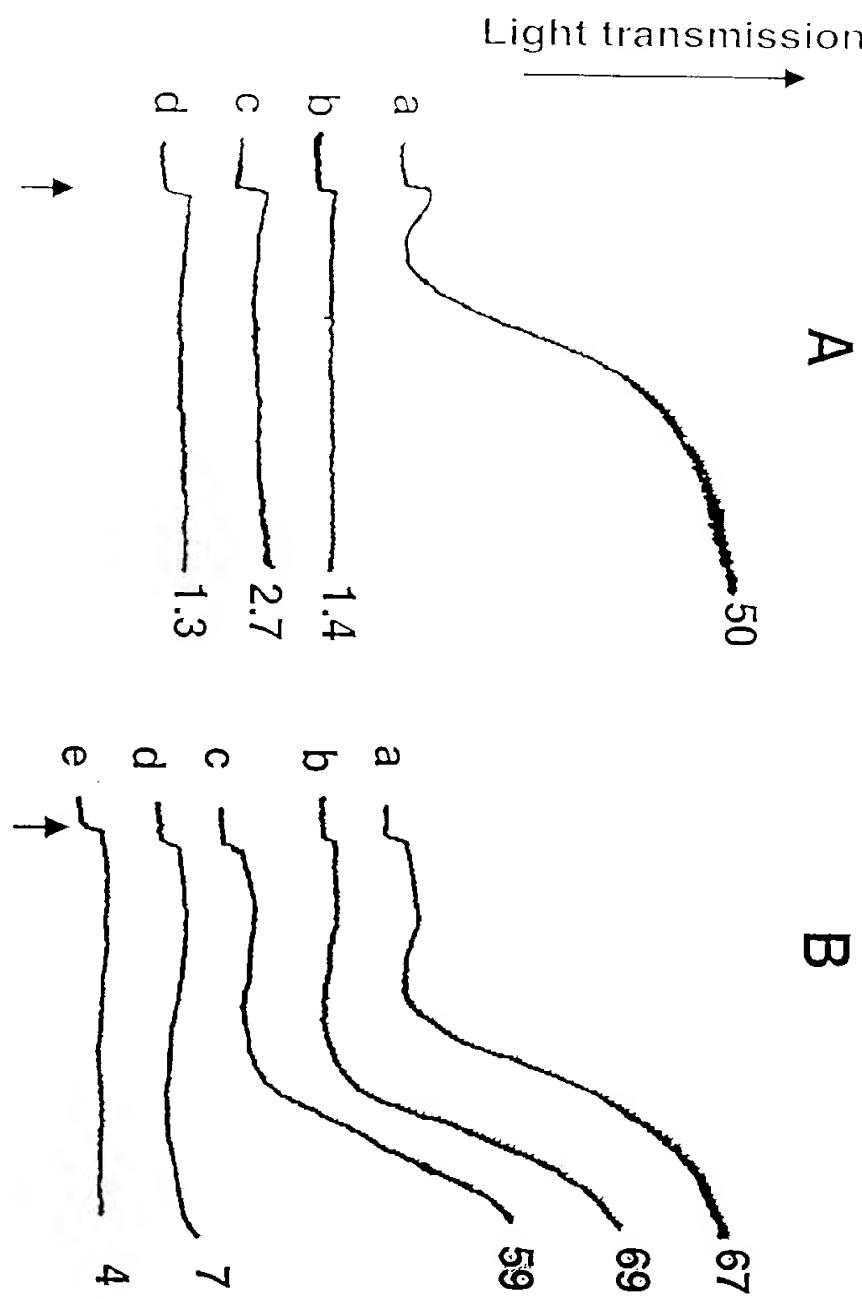


FIGURE 17

**FIGURE 18**

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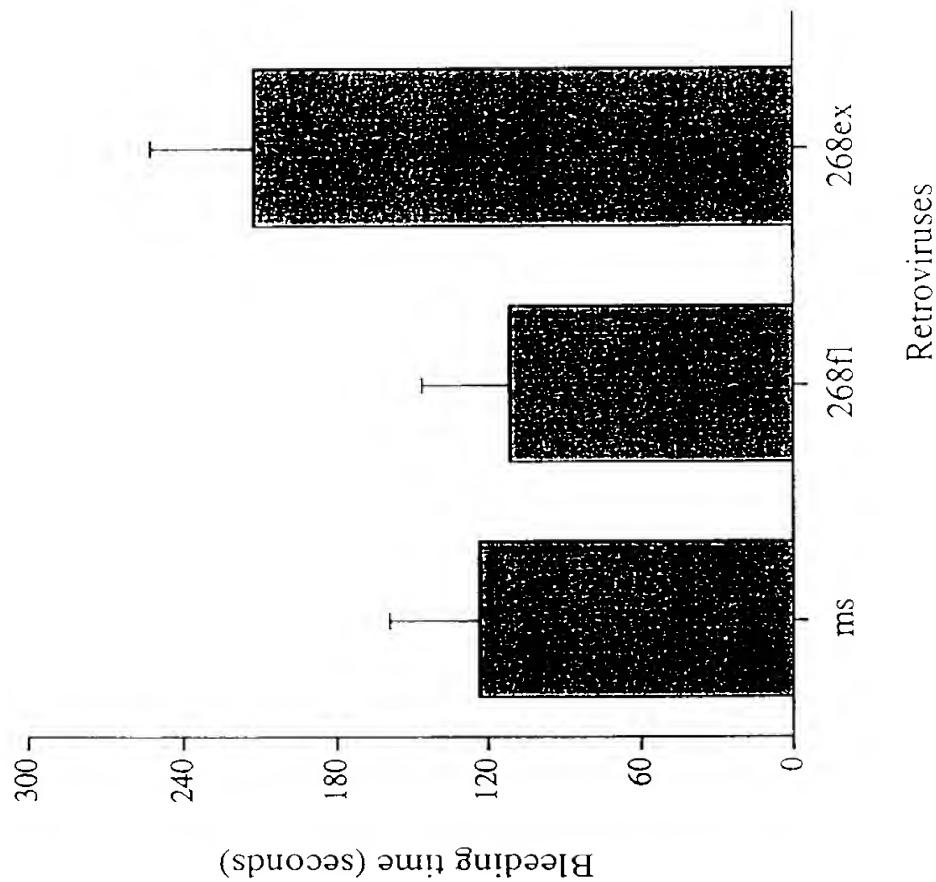


FIGURE 19